

RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



1653
TECH CENTER 1600/2900
RECEIVED
DEC 21 2001

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors while processing the following computer readable form:

Application Serial Number: 09/134,583

Source: C. P.

Date Processed by STIC: 9/16/2001

C/O ALLAN
FENUCCI

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§ 1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

mark.spencer@uspto.gov

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/734,583
ATTN: NEW RULES CASES: PLEASE DO NOT RE-ENTER ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics _____ Wrapped Amino	The number at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping".	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino _____ Numbering	The numbering for each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your submission is saved in ASCII text.	
5 _____ Variable Length.	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 _____ "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences previously submitted. Normally, PatentIn would automatically generate this section from the submitted nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (ii) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped. Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence identifier number <400> sequence identifier number 000	
9 _____ Use of n's or Xaa's (NEW RULES)	Use of n's or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220>-<223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 _____ Invalid <213> _____ Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or Scientific Name (Genus/Species). <220>-<223> section is required when <213> response is Unknown or Artificial Sequence.	
11 _____ Use of <220>.	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220>-<223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220>-<223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (See 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 _____ "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value specifically a nucleotide.	

#6
OIFERAW SEQUENCE ID NUMBER
PATENT APPLICATION: US/09/734,583DATE: 09/06/2001
TIME: 15:09:42Input Set : A:\P534-3000.txt
Output Set: N:\OUT3\09062001\I734583.rawDoes Not Comply
Corrected Diskette Needed3 <110> APPLICANT: Hornik, Vered
5 <120> TITLE OF INVENTION: CONFORMATIONALLY CONSTRAINED BACKBONE CYCLIZED SOMATOSTATIN

ANALOGS

7 <130> FILE REFERENCE: 87534-3000
9 <140> CURRENT APPLICATION NUMBER: 09/734,583
10 <141> CURRENT FILING DATE: 2000-12-13
12 <160> NUMBER OF SEQ ID NOS: 1
14 <170> SOFTWARE: PatentIn version 3.1
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 14
18 <212> TYPE: PRT
19 <213> ORGANISM: mammalian
21 <400> SEQUENCE: 1
23 Ala Gly Cys Lys Asn Phe Phe Trp Lys Thr Phe Thr Ser Cys
24 1 5 1025 <210> SEQ ID NO: 2
28 <211> LENGTH: 6
29 <212> TYPE: PRT
30 <213> ORGANISM: Artificial peptide
32 <220> FEATURE:
W--> 33 <221> NAME/KEY: DISULFIDE BRIDGE
34 <222> LOCATION: (1)..(1)
35 <223> OTHER INFORMATION: Cys residues at amino acid positions 1 and 6 form a disulfide

birdg

36
39 <220> FEATURE:
40 <221> NAME/KEY: MOD_RES
41 <222> LOCATION: (3)..(3)
42 <223> OTHER INFORMATION: The Trp residue is the D isomer
45 <400> SEQUENCE: 2
47 Cys Phe Trp Lys Thr Cys
48 1 551 <210> SEQ ID NO: 3
52 <211> LENGTH: 6
53 <212> TYPE: PRT
C--> 54 <213> ORGANISM: Artificial peptide
56 <220> FEATURE:
57 <221> NAME/KEY: MOD_RES
58 <222> LOCATION: (1)..(1)
59 <223> OTHER INFORMATION: N-Methyl
62 <220> FEATURE:
63 <221> NAME/KEY: MOD_RES
64 <222> LOCATION: (1)..(6)
65 <223> OTHER INFORMATION: cyclic
68 <220> FEATURE:
69 <221> NAME/KEY: MOD_RES
70 <222> LOCATION: (3)..(3)
71 <223> OTHER INFORMATION: The Trp residue is the D isomersee items 10 and 11 on Enin
summary
sheet
1?

same enin

74 <400> SEQUENCE: 3

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/734,583

DATE: 09/06/2001
TIME: 15:09:42

Input Set : A:\17514-3000.txt
Output Set : N:\REF1\09062001\1734583.raw

76 Ala Tyr Trp Lys Val Phe.
77 1 5
80 <210> SEQ ID NO: 4
81 <211> LENGTH: 8
82 <212> TYPE: PRT
C--> 83 <213> ORGANISM: Artificial Peptide
85 <220> FEATURE:
86 <221> NAME/KEY: MOD_RES
87 <222> LOCATION: (1)..(1)
88 <223> OTHER INFORMATION: The Phe residue is a D isomer
91 <220> FEATURE:
92 <221> NAME/KEY: MOD_RES
93 <222> LOCATION: (8)..(8)
94 <223> OTHER INFORMATION: The Thr residue ends with CH2OH
97 <220> FEATURE:
W--> 98 <221> NAME/KEY: DISULFIDE BRIDGE *bridge*
99 <222> LOCATION: (2)..(2)
100 <223> OTHER INFORMATION: A disulfide bridge is formed between Cys residues 2 and 7
103 <220> FEATURE:
104 <221> NAME/KEY: MOD_RES
105 <222> LOCATION: (2)..(2) *4? Cys is at location 2*
106 <223> OTHER INFORMATION: The Trp residue is a D isomer
109 <400> SEQUENCE: 4
111 Phe Cys Phe Trp Lys Thr Cys Thr
112 1 5
115 <210> SEQ ID NO: 5
116 <211> LENGTH: 7
117 <212> TYPE: PRT
C--> 118 <213> ORGANISM: Artificial Peptide *Artificial Sequence*
120 <220> FEATURE:
W--> 121 <221> NAME/KEY: DISULFIDE
122 <222> LOCATION: (2)..(2)
123 <223> OTHER INFORMATION: Disulfide Bridge is formed between the Cys residues at
position Synthetic 2 and 6
124 2 and 6
127 <220> FEATURE:
128 <221> NAME/KEY: MOD_RES
129 <222> LOCATION: (1)..(1)
130 <223> OTHER INFORMATION: The Phe residue is a D isomer
133 <220> FEATURE:
134 <221> NAME/KEY: MOD_RES
135 <222> LOCATION: (4)..(4)
136 <223> OTHER INFORMATION: The Trp residue is a D isomer
139 <220> FEATURE:
140 <221> NAME/KEY: MOD_RES
141 <222> LOCATION: (7)..(7)
142 <223> OTHER INFORMATION: The Thr residue ends with N2H
145 <400> SEQUENCE: 5
147 Phe Cys Phe Trp Lys Cys Thr
148 1 5

RAW SEQUENCE LISTING
PATENT APPLICATION: 118/09/734,583

DATE: 09/06/2001
TIME: 15:09:42

Input Set : A:\ 7534-1000.txt
Output Set : N:\ RF3\01062001\I734583.raw

151 <210> SEQ ID NO: 6
152 <211> LENGTH: 8
153 <212> TYPE: PRT
C--> 154 <213> ORGANISM: Artificial peptide
156 <220> FEATURE:
157 <221> NAME/KEY: MISC_FEATURE
158 <222> LOCATION: (1)..(1)
159 <223> OTHER INFORMATION: is a gamma amino butyric acid, diamino butyric acid, Gly,
beta-Ala
160 a, 5-amino pentanoic acid or amino hexanoic acid; Residue 1 is bridged
161 bridged to Residue 8; Residue 1 also begins with a hydrogen, or a
162 mono- or di- saccharide attached
165 <220> FEATURE:
166 <221> NAME/KEY: MISC_FEATURE
167 <222> LOCATION: (2)..(2)
168 <223> OTHER INFORMATION: is (D) or (L) Phe or Tyr
171 <220> FEATURE:
172 <221> NAME/KEY: MISC_FEATURE
173 <222> LOCATION: (3)..(3)
174 <223> OTHER INFORMATION: is (L) or (L)-Trp, or (L)-Phe, (D)- or (L)-1Nal or (D) or
(L)-2Na
175 1, or Tyr
178 <220> FEATURE:
179 <221> NAME/KEY: MISC_FEATURE
180 <222> LOCATION: (4)..(4)
181 <223> OTHER INFORMATION: is (D) or (L)-Trp
184 <220> FEATURE:
185 <221> NAME/KEY: MISC_FEATURE
186 <222> LOCATION: (5)..(5)
187 <223> OTHER INFORMATION: is (D) or (L)-Lys
190 <220> FEATURE:
191 <221> NAME/KEY: MISC_FEATURE
192 <222> LOCATION: (6)..(6)
193 <223> OTHER INFORMATION: is Thr, Gly, Abu, Ser, Cys, Val, (D) or (L)-Ala, or (D)- or
(L)-A
194 1a, or Tyr
197 <220> FEATURE:
198 <221> NAME/KEY: MISC_FEATURE
199 <222> LOCATION: (7)..(7)
200 <223> OTHER INFORMATION: is (D) or (L)-Phe, or (D)- or (L)-Ala, Nle, or Cys;
203 <220> FEATURE:
204 <221> NAME/KEY: MISC_FEATURE
205 <222> LOCATION: (8)..(8)
206 <223> OTHER INFORMATION: is Gly, Val, Leu, (D) or (L)-Phe, or 1Nal or 2Nal; with a
termina
207 1 carboxy acid, amine or alcohol group.
210 <400> SEQUENCE: 6
W--> 212 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
213 1 5
216 <210> SEQ ID NO: 7
217 <211> LENGTH: 7
218 <212> TYPE: PRT
C--> 219 <213> ORGANISM: Artificial Peptide

RAW SEQUENCE MAPPING
 PATENT APPLICATION: US/09/734,583

DATE: 09/06/2001
 TIME: 15:09:42

Input Set : A:\P534-3000.txt
 Output Set: N:\Crf3\9062001\I734583.raw

221 <220> FEATURE:
 222 <221> NAME/KEY: MISC_FEATURE
 223 <222> LOCATION: (1)..(1)
 224 <223> OTHER INFORMATION: is (D)- or (L)-Phe, or (D)- or (L)-Ala; wherein Residue 1 is
 bridged to Residue 6 a bridging group composed of 1 to 5 methyl space
 225 rs connected to an amide, thioether, thioester, or disulfide, fol
 226 lowed by 1 to 5 methyl spacers
 227
 230 <220> FEATURE:
 231 <221> NAME/KEY: MISC_FEATURE
 232 <222> LOCATION: (2)..(2)
 233 <223> OTHER INFORMATION: is Tyr or (D)- or (L)-Phe
 236 <220> FEATURE:
 237 <221> NAME/KEY: MISC_FEATURE
 238 <222> LOCATION: (3)..(3)
 239 <223> OTHER INFORMATION: is (L)- or (L)-Trp, (D)- or (L)-1Nal, or (D)- or (L)-2Nal
 242 <220> FEATURE:
 243 <221> NAME/KEY: MISC_FEATURE
 244 <222> LOCATION: (5)..(5)
 245 <223> OTHER INFORMATION: is Thr, Val, Ser, or Cys
 248 <220> FEATURE:
 249 <221> NAME/KEY: MISC_FEATURE
 250 <222> LOCATION: (6)..(6)
 251 <223> OTHER INFORMATION: is Gly or (D)- or (L)-Phe
 254 <220> FEATURE:
 255 <221> NAME/KEY: MISC_FEATURE
 256 <222> LOCATION: (7)..(7)
 257 <223> OTHER INFORMATION: is Thr, GABA, (D)- or (L)-1Nal, (D)- or (L)-2Nal, or (D)- or
 (L)-Phe
 258)-Phe
 261 <400> SEQUENCE: 7
 W--> 263 Xaa Xaa Xaa Lys Xaa Xaa Xaa
 264 1 5
 267 <210> SEQ ID NO: 8
 268 <211> LENGTH: 9
 269 <212> TYPE: PRT
 C--> 270 <213> ORGANISM: Artificial Peptide
 272 <220> FEATURE:
 273 <221> NAME/KEY: MISC_FEATURE
 274 <222> LOCATION: (1)..(1)
 275 <223> OTHER INFORMATION: is absent or is a terminal group of one to four amino acids
 278 <220> FEATURE:
 279 <221> NAME/KEY: MISC_FEATURE
 280 <222> LOCATION: (2)..(2)
 281 <223> OTHER INFORMATION: is 1Nal, 2Nal, Beta-Asp (Ind), Gly, Tyr, (D)- or (L)-Ala, or
 (D)- or (L)-Phe
 282)- or (L)-Phe
 285 <220> FEATURE:
 286 <221> NAME/KEY: MISC_FEATURE
 287 <222> LOCATION: (3)..(4)
 288 <223> OTHER INFORMATION: may be absent, or are independently Gly, Tyr, 1Nal, 2Nal,
 Beta-Asp
 289 p (Ind), Gly, Tyr, (D)- or (L)-Ala, or (D)- or (L)-Phe

see item 5 on Error Summary Sheet
variable length invalid

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/734,583

DATE: 09/06/2001
TIME: 15:09:42

Input Set : A:\734-0000.txt
Output Set : N:\CRF3\00062001\I734583.raw

292 <220> FEATURE:
293 <221> NAME/KEY: MISC_FEATURE
294 <222> LOCATION: (5)..(5)
295 <223> OTHER INFORMATION: (D) - or (L)-Trp
298 <220> FEATURE:
299 <221> NAME/KEY: MISC_FEATURE
300 <222> LOCATION: (6)..(6)
301 <223> OTHER INFORMATION: (D) - or (L)-Lys
304 <220> FEATURE:
305 <221> NAME/KEY: MISC_FEATURE
306 <222> LOCATION: (7)..(7)
307 <223> OTHER INFORMATION: is absent or is Gly, Abu, Cys, Thr, Val, (D)- or (L)-Ala, or
(D)
308 - or (L)-Phe
311 <220> FEATURE:
312 <221> NAME/KEY: MISC_FEATURE
313 <222> LOCATION: (8)..(8)
314 <223> OTHER INFORMATION: is (Cys, (D)- or (L)-Ala, or (D)- or (L)-Phe
317 <220> FEATURE:
318 <221> NAME/KEY: MISC_FEATURE
319 <222> LOCATION: (9)..(9)
320 <223> OTHER INFORMATION: is absent or is Val, Thr, 1Nal or 2Nal
323 <220> SEQUENCE: 8
W--> 325 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
326 1 5
329 <210> SEQ ID NO: 9
330 <211> LENGTH: 7
331 <212> TYPE: PRT
C--> 332 <213> ORGANISM: Artificial Peptide
334 <220> FEATURE:
335 <221> NAME/KEY: MISC_FEATURE
336 <222> LOCATION: (1)..(1)
337 <223> OTHER INFORMATION: (D)- or (L)-Phe, Tyr or (D)- or (L)-Ala; Residue 1 is
connected
338 to Residue 7 by a bridge comprised of 1 to 5 methylene spacers (C) Connected
339 connected to an amide, thioether, thioester, or disulfide, followed
340 d by 1 to 5 methylene spacers
343 <220> FEATURE:
344 <221> NAME/KEY: MISC_FEATURE
345 <222> LOCATION: (2)..(2)
346 <223> OTHER INFORMATION: (D)- or (L)-Phe, Tyr or (D)- or (L)-Ala;
349 <220> FEATURE:
350 <221> NAME/KEY: MISC_FEATURE
351 <222> LOCATION: (3)..(3)
352 <223> OTHER INFORMATION: is absent or is (D)- or (L)-Phe, Tyr or (D)- or (L)-Ala;
355 <220> FEATURE:
356 <221> NAME/KEY: MISC_FEATURE
357 <222> LOCATION: (4)..(4)
358 <223> OTHER INFORMATION: is (D)- or (L)-Tyr
361 <220> FEATURE:
362 <221> NAME/KEY: MISC_FEATURE

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/734,583DATE: 09/06/2001
TIME: 15:09:43Input Set : A:\I7514-3000.txt
Output Set: N:\TEMP\09062001\I734583.raw

L:30 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:33 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:54 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:83 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:98 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:118 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:121 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:154 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:212 M:341 W: (46) "n" or "Xaa" used for SEQ ID#:6 ←
L:219 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:263 M:341 W: (46) "n" or "Xaa" used for SEQ ID#:7
L:270 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:325 M:341 W: (46) "n" or "Xaa" used for SEQ ID#:8 ←
L:332 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:381 M:341 W: (46) "n" or "Xaa" used for SEQ ID#:9
L:388 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:437 M:341 W: (46) "n" or "Xaa" used for SEQ ID#:10 ←



UNITED STATES DEPARTMENT OF COMMERCE
Patent and Trademark Office

COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.

EXAMINER	
ART. UNIT	PAPER NUMBER

DATE MAILED:

Please find below a communication from the EXAMINER in charge of this application
Commissioner of Patents

1. This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). A computer readable form (CRF) of the sequence listing was submitted. However, the CRF could not be processed by the Scientific and Technical Information Center (STIC) for the reason(s) set forth on the attached CRF Diskette Problem Report. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) before the application can be examined under 35 U.S.C. §§ 131 and 132.

Applicant is given ONE MONTH from the mailing date of this communication within which to comply with the sequence rules, 37 CFR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136(a). Direct the reply to the undersigned. Applicant is requested to return a copy of the attached CRF Diskette Problem Report with the reply.


Anish Gupta

Application No.: 02/734,583**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 C.F.R. 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 3620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."
- ☒ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

COUNT SHEET FOR SEQUENCE CASES

Serial No. 09/734,583

AE _____

Date of Count _____

Mark only one space below

 X (CRFN) (CRF is unreadable; use CRF Diskette
Problem Report)

(CIFE) (CRF does not comply; use Notice to
Comply)

(CFFF) (CRF required but none submitted;
use Notice to Comply)

(bona fide) (second or subsequent letter to applicant
reporting bona fide attempt to comply;
use Notice to Comply and send copy of RSL)

(non bona fide) (second or subsequent letter to
applicant reporting non-bona fide
attempt to comply; use Notice to
Comply and send copy of RSL)Examiner Anish GuptaGAU 1653

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BEST AVAILABLE IMAGES

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- ☐ **BLURRED OR ILLEGIBLE TEXT OR DRAWING**
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- ☐ **OTHER: _____**

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